In the Claims:

1. (Original) A method, comprising:

a) providing a biological sample from a subject, said biological sample comprising genomic DNA;

b) detecting the presence or absence of DNA methylation in one or more genes to generate a methylation profile for said subject; and

c) comparing said methylation profile to one or more standard methylation profiles, wherein said standard methylation profiles are selected from the group consisting of methylation profiles of non cancerous samples and methylation profiles of cancerous samples.

2. (Original) The method of Claim 1, wherein said detecting the presence or absence of DNA methylation comprises the digestion of said genomic DNA with a methylation-sensitive restriction enzyme followed by multiplexed amplification of gene-specific DNA fragments with CpG islands.

3. (Currently amended) A method of characterizing cancer, comprising:

a) providing a biological sample from a subject diagnosed with cancer, said biological sample comprising genomic DNA; and

b) detecting the presence or absence of DNA methylation in each of DAPK, GSTP, p15, MDR1, Progesterone Receptor, Calcitonin, RIZ, and RARbeta genes to generate a profile, thereby characterizing cancer in said subject.

4. (Original) The method of claim 3, further comprising the step of detecting the presence or absence of DNA methylation in one or more genes selected from the group consisting of S100, SRBC, BRCA, HIN1, Cyclin D2, TMS1, HIC-1, hMLH1E-cadherin, 14-3-3sigma, and MDGI.

5. (Original) The method of claim 3, wherein said characterizing cancer comprises detecting the presence or absence of chemotherapy resistant cancer.

6. (Original) The method of claim 5, wherein said chemotherapy is a nonsteroidal selective estrogen receptor modulator.

7. (Original) The method of claim 3, wherein said characterizing cancer comprises determining a chance of disease-free survival.

8. (Original) The method of claim 3, wherein said characterizing cancer comprises determining the risk of developing metastatic disease.

9. (Original) The method of claim 3, wherein said characterizing cancer comprises monitoring disease progression in said subject.

10. (Original) The method of claim 3, wherein said biological sample is a biopsy sample.

11. (Original) The method of claim 3, wherein said biological sample is a blood sample.

12. (Original) The method of claim 3, wherein said DNA methylation comprises CpG methylation.

13. (Original) The method of claim 3, wherein said detecting the presence or absence of DNA methylation comprises the digestion of said genomic DNA with a methylation-sensitive restriction enzyme followed by multiplexed amplification of gene-specific DNA fragments with CpG islands.

14. (Original) The method of claim 13, wherein said methylation-sensitive restriction enzyme comprises Hin6I.

15. (Original) The method of claim 3, wherein said cancer is breast cancer.

16-20. (canceled)

21. (Previously presented) The method of claim 1, wherein said biological sample is a

biopsy sample.

22. (Previously presented) The method of claim 1, wherein said biological sample is a blood sample.

23. (Previously presented) The method of claim 1, wherein said DNA methylation comprises CpG methylation.

24. (Previously presented) The method of claim 1, wherein said cancer is breast cancer.